

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Beach, David H.
Demetrick, Douglas J.
Serrano, Manuel
Hannon, Gregory J.

(ii) TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and
Uses Related Thereto

(iii) NUMBER OF SEQUENCES: 35

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: Boston
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(E) COUNTRY: USA
(F) ZIP: 02110

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WordPad

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/016,869
(B) FILING DATE: 30-JAN-1998

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/893,274
(B) FILING DATE: 15-JUL-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/306,511
(B) FILING DATE: 14-SEP-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/248,812
(B) FILING DATE: 25-MAY-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/227,371
(B) FILING DATE: 14-APR-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/154,915
(B) FILING DATE: 18-NOV-1993

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/991,997
(B) FILING DATE: 17-DEC-1992

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Vincent, Matthew P.
(B) REGISTRATION NUMBER: 36,709

(C) REFERENCE/DOCKET NUMBER: GPCI-P10-071

(ix) TELECOMMUNICATION INFORMATION:

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(B) TELEFAX: (617) 951-7050

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 994 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 41..508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGGAGAGGGG GAGAACAGAC AACGGGCGGC GGGGAGCAGC ATG GAT CCG GCG GCG 55
Met Asp Pro Ala Ala
1 5
GGG AGC AGC ATG GAG CCT TCG GCT GAC TGG CTG GCC ACG GCC GCG GCC 103
Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu Ala Thr Ala Ala Ala
10 15 20
CGG GGT CGG GTA GAG GAG GTG CGG GCG CTG CTG GAG GCG GTG GCG CTG 151
Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu Glu Ala Val Ala Leu
25 30 35
CCC AAC GCA CCG AAT AGT TAC GGT CGG AGG CCG ATC CAG GTC ATG ATG 199
Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro Ile Gln Val Met Met
40 45 50
ATG GGC AGC GCC CGA GTG GCG GAG CTG CTG CTG CTC CAC GGC GCG GAG 247
Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu His Gly Ala Glu
55 60 65
CCC AAC TGC GCC GAC CCC GCC ACT CTC ACC CGA CCC GTG CAC GAC GCT 295
Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val His Asp Ala
70 75 80 85
GCC CGG GAG GGC TTC CTG GAC ACG CTG GTG GTG CTG CAC CGG GCC GGG 343
Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Leu His Arg Ala Gly
90 95 100
GCG CGG CTG GAC GTG CGC GAT GCC TGG GGC CGT CTG CCC GTG GAC CTG 391
Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu
105 110 115
GCT GAG GAG CTG GGC CAT CGC GAT GTC GCA CGG TAC CTG CGC GCG GCT 439
Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg Tyr Leu Arg Ala Ala
120 125 130
GCG GGG GGC ACC AGA GGC AGT AAC CAT GCC CGC ATA GAT GCC GCG GAA 487
Ala Gly Gly Thr Arg Gly Ser Asn His Ala Arg Ile Asp Ala Ala Glu
135 140 145
GGT CCC TCA GAC ATC CCC GAT TGAAAGAACC AGAGAGGCTC TGAGAAACCT 538
Gly Pro Ser Asp Ile Pro Asp
150 155
CGGGAAACTT AGATCATCAG TCACCGAAGG TCCTACAGGG CCACAACCTGC CCCC GCCACA 598
ACCCACCCCG CTTTCGTAGT TTTCATTTAG AAAATAGAGC TTTTAAAAAT GTCCTGCCTT 658
TTAACGTAGA TATAAGCCTT CCCCCACTAC CGTAAATGTC CATTTATATC ATTTTATATA 718
TATTCTTATA AAAATGTAAA AAAGAAAAAC ACCGCTTCTG CCTTTTCACT GTGTTGGAGT 778
TTTCTGGAGT GAGCACTCAC GCCCTAAGCG CACATTCATG TGGGCATTTC TTGCGAGCCT 838
CGCAGCCTCC GGAAGCTGTC GACTTCATGA CAAGCATTTT GTGAACTAGG GAAGCTCAGG 898
GGGGTTACTG GCTTCTCTTG AGTCACACTG CTAGCAAATG GCAGAACCAA AGCTCAAATA 958

AAAATAAAAT TATTTTCATT CATTCACTCA AAAAAA

994

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Asp Pro Ala Ala Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu
 1          5          10          15
Ala Thr Ala Ala Ala Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu
 20          25          30
Glu Ala Val Ala Leu Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro
 35          40          45
Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu
 50          55          60
Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg
 65          70          75          80
Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val
 85          90          95
Leu His Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg
100          105          110
Leu Pro Val Asp Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg
115          120          125
Tyr Leu Arg Ala Ala Ala Gly Gly Thr Arg Gly Ser Asn His Ala Arg
130          135          140
Ile Asp Ala Ala Glu Gly Pro Ser Asp Ile Pro Asp
145          150          155

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 328..738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

GAGGACTCCG CGACGGTCCG CACCCTGCGG CCAGAGCGGC TTTGAGCTCG GCTGCTTCCG      60
CGCTAGGCGC TTTTTCAGAG AAGCAATCCA GCGCGCCCCG CTGGTTCTTG AGCGCCAGGA      120
AAAGCCCGGA GCTAACGACC GGCCGCTCGG CACTGCACGG GGCCCAAGC CGCAGAAGAA      180
GGACGACGGG AGGGTAATGA AGCTGAGCCC AGGTCTCCTA GGAAGGAGAG AGTGCGCCGG      240
AGCAGCGTGG GAAAGAAGGG AAGAGTGTCT TTAAGTTTAC GGCCAACGGT GGATTATCCG      300
GGCCGCTGCG CGTCTGGGGG CTGCGGGA ATG CGC GAG GAG AAC AAG GGC ATG      351
                Met Arg Glu Glu Asn Lys Gly Met
                1          5
CCC AGT GGG GGC GGC AGC GAT GAG GGT CTG GCC ACG CCG GCG CGG GGA      399
Pro Ser Gly Gly Gly Ser Asp Glu Gly Leu Ala Thr Pro Ala Arg Gly
 10          15          20
CTA GTG GAG AAG GTG CGA CAC TCC TGG GAA GCC GGC GCG GAT CCC AAC      447

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Leu	Val	Glu	Lys	Val	Arg	His	Ser	Trp	Glu	Ala	Gly	Ala	Asp	Pro	Asn	
25					30					35					40	
GGA	GTC	AAC	CGT	TTC	GGG	AGG	CGC	GCG	ATC	CAG	GTC	ATG	ATG	ATG	GGC	495
Gly	Val	Asn	Arg	Phe	Gly	Arg	Arg	Ala	Ile	Gln	Val	Met	Met	Met	Gly	
			45						50					55		
AGC	GCC	CGC	GTG	GCG	GAG	CTG	CTG	CTG	CTC	CAC	GGC	GCG	GAG	CCC	AAC	543
Ser	Ala	Arg	Val	Ala	Glu	Leu	Leu	Leu	His	Gly	Ala	Glu	Pro	Asn		
			60					65					70			
TGC	GCA	GAC	CCT	GCC	ACT	CTC	ACC	CGA	CCG	GTG	CAT	GAT	GCT	GCC	CGG	591
Cys	Ala	Asp	Pro	Ala	Thr	Leu	Thr	Arg	Pro	Val	His	Asp	Ala	Ala	Arg	
		75					80					85				
GAG	GGC	TTC	CTG	GAC	ACG	CTG	GTG	GTG	CTG	CAC	CGG	GCC	GGG	GCG	CGG	639
Glu	Gly	Phe	Leu	Asp	Thr	Val	Val	Val	Leu	His	Arg	Ala	Gly	Ala	Arg	
		90				95					100					
CTG	GAC	GTG	CGC	GAT	GCC	TGG	GGT	CGT	CTG	CCC	GTG	GAC	TTG	GCC	GAG	687
Leu	Asp	Val	Arg	Asp	Ala	Trp	Gly	Arg	Leu	Pro	Val	Asp	Leu	Ala	Glu	
		105			110					115				120		
GAG	CGG	GGC	CAC	CGC	GAC	GTT	GCA	GGG	TAC	CTG	CGC	ACA	GCC	ACG	GGG	735
Glu	Arg	Gly	His	Arg	Asp	Val	Ala	Gly	Tyr	Leu	Arg	Thr	Ala	Thr	Gly	
			125					130					135			
GAC	TGACGCCAGG	TTCCCCAGCC	GCCCCACAACG	ACTTTATTTT	CTTACCCAAT											788
Asp																
TTCCACCCCC	CACCCACCTA	ATTCGATGAA	GGCTGCCAAC	GGGGAGCGG												837

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Arg	Glu	Glu	Asn	Lys	Gly	Met	Pro	Ser	Gly	Gly	Gly	Ser	Asp	Glu
1				5					10					15	
Gly	Leu	Ala	Thr	Pro	Ala	Arg	Gly	Leu	Val	Glu	Lys	Val	Arg	His	Ser
			20					25					30		
Trp	Glu	Ala	Gly	Ala	Asp	Pro	Asn	Gly	Val	Asn	Arg	Phe	Gly	Arg	Arg
		35					40					45			
Ala	Ile	Gln	Val	Met	Met	Met	Gly	Ser	Ala	Arg	Val	Ala	Glu	Leu	Leu
	50					55					60				
Leu	Leu	His	Gly	Ala	Glu	Pro	Asn	Cys	Ala	Asp	Pro	Ala	Thr	Leu	Thr
	65				70					75				80	
Arg	Pro	Val	His	Asp	Ala	Ala	Arg	Glu	Gly	Phe	Leu	Asp	Thr	Leu	Val
			85					90					95		
Val	Leu	His	Arg	Ala	Gly	Ala	Arg	Leu	Asp	Val	Arg	Asp	Ala	Trp	Gly
			100					105					110		
Arg	Leu	Pro	Val	Asp	Leu	Ala	Glu	Glu	Arg	Gly	His	Arg	Asp	Val	Ala
		115					120					125			
Gly	Tyr	Leu	Arg	Thr	Ala	Thr	Gly	Asp							
	130					135									

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 853 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 213..587

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGAGTACAGC AGCGGGAGCA TGGGTCGCAG GTTCTTGGTC ACTGTAAGGA TTCAGCGCGC	60
GGGCCGCCCA CTCCAAGAGA GGGTTTTCTT GGTGAAGTTC GTGCGATCCC GGAGACCCAG	120
GACAGCGAGC TCGCCTCTGG CTTTCGTGAA CATGTTGTTG AGGCTAGAGA GGATCTTGAG	180
AAGAGGGCCG CACCGGAATC CTGGACCAGG TG ATG ATG ATG GGC AAC GTT CAC	233
Met Met Met Gly Asn Val His	
1 5	
GTA GCA GCT CTT CTG CTC AAC TAC GGT GCA GAT TCG AAC TGC GAG GAC	281
Val Ala Ala Leu Leu Leu Asn Tyr Gly Ala Asp Ser Asn Cys Glu Asp	
10 15 20	
CCC ACT ACC TTC TCC CGC CCG GTG CAC GAC GCA GCG CGG GAA GGC TTC	329
Pro Thr Thr Phe Ser Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe	
25 30 35	
CTG GAC ACG CTG GTG GTG CTG CAC GGG TCA GGG GCT CGG CTG GAT GTG	377
Leu Asp Thr Leu Val Val Leu His Gly Ser Gly Ala Arg Leu Asp Val	
40 45 50 55	
CGC GAT GCC TGG GGT CGC CTG CCG CTC GAC TTG GCC CAA GAG CGG GGA	425
Arg Asp Ala Trp Gly Arg Leu Pro Leu Asp Leu Ala Gln Glu Arg Gly	
60 65 70	
CAT CAA GAC ATC GTG CGA TAT TTG CGT TCC GCT GGG TGC TCT TTG TGT	473
His Gln Asp Ile Val Arg Tyr Leu Arg Ser Ala Gly Cys Ser Leu Cys	
75 80 85	
TCC GCT GGG TGG TCT TTG TGT ACC GCT GGG AAC GTC GCC CAG ACC GAC	521
Ser Ala Gly Trp Ser Leu Cys Thr Ala Gly Asn Val Ala Gln Thr Asp	
90 95 100	
GGG CAT AGC TTC AGC TCA AGC ACG CCC AGG GCC CTG GAA CTT CGC GGC	569
Gly His Ser Phe Ser Ser Ser Thr Pro Arg Ala Leu Glu Leu Arg Gly	
105 110 115	
CAA TCC CAA GAG CAG AGC TAAATCCGCC TCAGCCCGCC TTTTCTTCT	617
Gln Ser Gln Glu Gln Ser	
120 125	
TAGCTTCACT TCTAGCGATG CTAGCGTGTC TAGCATGTGG CTTTAAAAAA TACATAATAA	677
TGCTTTTTTTT GCAATCACGG GAGGGAGCAG AGGGAGGGAG CAGAAGGAGG GAGGGAGGGA	737
GGGAGGGACC TGGACAGGAA AGGAATGGCA TGAGAACTG AGCGAAGGCG GCCGCGAAGG	797
GAATAATGGC TGGATTGTTT AAAAAAATAA AATAAAGATA CTTTTTAAAA TGTCAA	853

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Met	Met	Gly	Asn	Val	His	Val	Ala	Ala	Leu	Leu	Leu	Asn	Tyr	Gly	
1				5					10					15		
Ala	Asp	Ser	Asn	Cys	Glu	Asp	Pro	Thr	Thr	Phe	Ser	Arg	Pro	Val	His	
	20						25						30			
Asp	Ala	Ala	Arg	Glu	Gly	Phe	Leu	Asp	Thr	Leu	Val	Val	Leu	His	Gly	
	35					40					45					
Ser	Gly	Ala	Arg	Leu	Asp	Val	Arg	Asp	Ala	Trp	Gly	Arg	Leu	Pro	Leu	
	50				55					60						
Asp	Leu	Ala	Gln	Glu	Arg	Gly	His	Gln	Asp	Ile	Val	Arg	Tyr	Leu	Arg	
	65				70				75					80		
Ser	Ala	Gly	Cys	Ser	Leu	Cys	Ser	Ala	Gly	Trp	Ser	Leu	Cys	Thr	Ala	
			85						90					95		
Gly	Asn	Val	Ala	Gln	Thr	Asp	Gly	His	Ser	Phe	Ser	Ser	Ser	Thr	Pro	
	100						105						110			
Arg	Ala	Leu	Glu	Leu	Arg	Gly	Gln	Ser	Gln	Glu	Gln	Ser				
	115					120						125				

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCA	CTC	CTG	GAA	GCC	GGC	GCA	GAT	CCC	AAC	GCC	CTG	AAC	CGC	TTC	GGG	48
Ala	Leu	Leu	Glu	Ala	Gly	Ala	Asp	Pro	Asn	Ala	Leu	Asn	Arg	Phe	Gly	
1				5					10					15		
AGG	CGC	CCA	ATC	CAG	GTC	ATG	ATG	ATG	GGC	AGC	GCC	AGG	GTG	GCA	GAG	96
Arg	Arg	Pro	Ile	Gln	Val	Met	Met	Met	Gly	Ser	Ala	Arg	Val	Ala	Glu	
			20					25					30			
CTG	CTG	CTG	CTC	CAC	GGA	GCA	GAA	CCC	AAC	TGC	GCC	GAC	CCT	GCC	ACC	144
Leu	Leu	Leu	Leu	His	Gly	Ala	Glu	Pro	Asn	Cys	Ala	Asp	Pro	Ala	Thr	
			35				40					45				
CTT	ACC	AGA	CCT	GTG	CAC	GAC	GCA	GCT	CGG	GAA	GGC	TTC	CTG	GAC	ACG	192

Leu Thr Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr
 50 55 60
 CTT GTC GTG CTG CAC CGG GCA GGG GCG CGG TTG GAT GTG
 Leu Val Val Leu His Arg Ala Gly Ala Arg Leu Asp Val
 65 70 75

231

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 77 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala Leu Leu Glu Ala Gly Ala Asp Pro Asn Ala Leu Asn Arg Phe Gly
 1 5 10 15
 Arg Arg Pro Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu
 20 25 30
 Leu Leu Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr
 35 40 45
 Leu Thr Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr
 50 55 60
 Leu Val Val Leu His Arg Ala Gly Ala Arg Leu Asp Val
 65 70 75

(2) INFORMATION FOR SEQ ID NO:9:

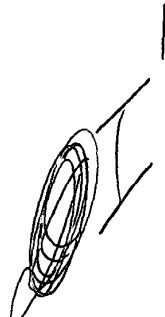
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 303 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ala Thr Ser Arg Tyr Glu Pro Val Ala Glu Ile Gly Val Gly Ala
 1 5 10 15
 Tyr Gly Thr Val Tyr Lys Ala Xaa Asp Pro His Ser Gly His Phe Val
 20 25 30
 Ala Leu Lys Ser Val Arg Val Pro Asn Gly Gly Gly Gly Gly Gly Gly
 35 40 45
 Leu Pro Ile Ser Thr Val Arg Glu Val Ala Leu Leu Arg Arg Leu Glu
 50 55 60
 Ala Phe Glu His Pro Asn Val Val Arg Leu Met Asp Val Cys Ala Thr
 65 70 75 80



Ser	Arg	Thr	Asp	Arg	Glu	Ile	Lys	Val	Thr	Leu	Val	Phe	Glu	His	Val
				85					90					95	
Asp	Gln	Asp	Leu	Arg	Thr	Tyr	Leu	Asp	Lys	Ala	Pro	Pro	Pro	Gly	Leu
			100					105						110	
Pro	Ala	Glu	Thr	Ile	Lys	Asp	Leu	Met	Arg	Gln	Phe	Leu	Arg	Gly	Leu
			115				120					125			
Asp	Phe	Leu	His	Ala	Asn	Cys	Ile	Val	His	Arg	Asp	Leu	Lys	Pro	Glu
			130			135					140				
Asn	Ile	Leu	Val	Thr	Ser	Gly	Gly	Thr	Val	Lys	Leu	Ala	Asp	Phe	Gly
					150					155					160
Leu	Ala	Arg	Ile	Tyr	Ser	Tyr	Gln	Met	Ala	Leu	Thr	Pro	Val	Val	Val
				165					170					175	
Thr	Leu	Trp	Tyr	Arg	Ala	Pro	Glu	Val	Leu	Leu	Gln	Ser	Thr	Tyr	Ala
			180					185					190		
Thr	Pro	Val	Asp	Met	Trp	Ser	Val	Gly	Cys	Ile	Phe	Ala	Glu	Met	Phe
			195				200					205			
Arg	Arg	Lys	Pro	Leu	Phe	Cys	Gly	Asn	Ser	Glu	Ala	Asp	Gln	Leu	Gly
			210			215					220				
Lys	Ile	Phe	Asp	Leu	Ile	Gly	Leu	Pro	Pro	Glu	Asp	Asp	Trp	Pro	Arg
					230					235					240
Asp	Val	Ser	Leu	Pro	Arg	Gly	Ala	Phe	Pro	Pro	Arg	Gly	Pro	Arg	Pro
				245					250					255	
Val	Gln	Ser	Val	Val	Pro	Glu	Met	Glu	Glu	Ser	Gly	Ala	Gln	Leu	Leu
				260				265					270		
Leu	Glu	Met	Leu	Thr	Phe	Asn	Pro	His	Lys	Arg	Ile	Ser	Ala	Phe	Arg
			275				280					285			
Ala	Leu	Gln	His	Ser	Tyr	Leu	His	Lys	Asp	Glu	Gly	Asn	Pro	Glu	
			290			295					300				

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Glu	Lys	Asp	Gly	Leu	Cys	Arg	Ala	Asp	Gln	Gln	Tyr	Glu	Cys	Val
1				5				10					15		
Ala	Glu	Ile	Gly	Glu	Gly	Ala	Tyr	Gly	Lys	Val	Phe	Lys	Ala	Xaa	Asp

20	25	30
Leu Lys Asn Gly Gly Arg Phe Val Ala Leu Lys Arg Val Arg Val Gln		
35	40	45
Thr Gly Glu Glu Gly Met Pro Leu Ser Thr Ile Arg Glu Val Ala Val		
50	55	60
Leu Arg His Leu Glu Thr Phe Glu His Pro Asn Val Val Arg Leu Phe		
65	70	75
Asp Val Cys Thr Val Ser Arg Thr Asp Arg Glu Thr Lys Leu Thr Leu		
85	90	95
Val Phe Glu His Val Asp Gln Asp Leu Thr Thr Tyr Leu Asp Lys Val		
100	105	110
Pro Glu Pro Gly Val Pro Thr Glu Thr Ile Lys Asp Met Met Phe Gln		
115	120	125
Leu Leu Arg Gly Leu Asp Phe Leu His Ser His Arg Val Val His Arg		
130	135	140
Asp Leu Lys Pro Gln Asn Ile Leu Val Thr Ser Ser Gly Gln Ile Lys		
145	150	155
Leu Ala Asp Phe Gly Leu Ala Arg Ile Tyr Ser Phe Gln Met Ala Leu		
165	170	175
Thr Ser Val Val Val Thr Leu Trp Tyr Arg Ala Pro Glu Val Leu Leu		
180	185	190
Gln Ser Ser Tyr Ala Thr Pro Val Asp Leu Trp Ser Val Gly Cys Ile		
195	200	205
Phe Ala Glu Met Phe Arg Arg Lys Pro Leu Phe Arg Gly Ser Ser Asp		
210	215	220
Val Asp Gln Leu Gly Lys Ile Leu Asp Val Ile Gly Leu Pro Gly Glu		
225	230	235
Glu Asp Trp Pro Arg Asp Val Ala Leu Pro Arg Gln Ala Phe His Ser		
245	250	255
Lys Ser Ala Gln Pro Ile Glu Lys Phe Val Thr Asp Ile Asp Glu Leu		
260	265	270
Gly Lys Asp Leu Leu Leu Lys Cys Leu Thr Phe Asn Pro Ala Lys Arg		
275	280	285
Ile Ser Ala Tyr Ser Ala Leu Ser His Pro Tyr Phe Gln Asp Leu Glu		
290	295	300
Arg Cys Lys Glu Asn Leu Asp Ser His Leu Pro Pro Ser Gln Asn Thr		
305	310	315
Ser Glu Leu Asn Thr Ala		
325		

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 85 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Met Met Gly Xaa Xaa Xaa Val Ala Xaa Leu Leu Leu Xaa Xaa Gly
 1 5 10 15
 Ala Xaa Xaa Asn Cys Xaa Asp Pro Xaa Thr Xaa Xaa Xaa Arg Pro Val
 20 25 30
 His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His
 35 40 45
 Xaa Xaa Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro
 50 55 60
 Xaa Asp Leu Ala Xaa Glu Xaa Gly His Xaa Asp Xaa Xaa Xaa Tyr Leu
 65 70 75 80
 Arg Xaa Ala Xaa Gly
 85

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 157 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Asp Pro Ala Ala Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu
 1 5 10 15
 Ala Thr Ala Ala Ala Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu
 20 25 30
 Glu Ala Val Ala Leu Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro
 35 40 45
 Ile Gln Val Met Met Met Gly Xaa Xaa Xaa Val Ala Xaa Leu Leu Leu
 50 55 60

Xaa Xaa Gly Ala Xaa Xaa Asn Cys Xaa Asp Pro Xaa Thr Xaa Xaa Xaa
65 70 75 80

Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val
85 90 95

Val Leu His Xaa Xaa Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly
100 105 110

Arg Leu Pro Xaa Asp Leu Ala Xaa Glu Xaa Gly His Xaa Asp Xaa Xaa
115 120 125

Xaa Tyr Leu Arg Xaa Ala Xaa Gly Gly Thr Arg Gly Ser Asn His Ala
130 135 140

Arg Ile Asp Ala Ala Glu Gly Pro Ser Asp Ile Pro Asp
145 150 155

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Arg Glu Glu Asn Lys Gly Met Pro Ser Gly Gly Gly Ser Asp Glu
1 5 10 15

Gly Leu Ala Thr Pro Ala Arg Gly Leu Val Glu Lys Val Arg His Ser
20 25 30

Trp Glu Ala Gly Ala Asp Pro Asn Gly Val Asn Arg Phe Gly Arg Arg
35 40 45

Ala Ile Gln Val Met Met Met Gly Xaa Xaa Xaa Val Ala Xaa Leu Leu
50 55 60

Leu Xaa Xaa Gly Ala Xaa Xaa Asn Cys Xaa Asp Pro Xaa Thr Xaa Xaa
65 70 75 80

Xaa Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu
85 90 95

Val Val Leu His Xaa Xaa Gly Ala Arg Leu Asp Val Arg Asp Ala Trp
100 105 110

Gly Arg Leu Pro Xaa Asp Leu Ala Xaa Glu Xaa Gly His Xaa Asp Xaa
115 120 125

Xaa Xaa Tyr Leu Arg Xaa Ala Xaa Gly Asp
130 135

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 127 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Met Met Gly Xaa Xaa Xaa Val Ala Xaa Leu Leu Leu Xaa Xaa Gly
1 5 10 15

Ala Xaa Xaa Asn Cys Xaa Asp Pro Xaa Thr Xaa Xaa Xaa Arg Pro Val
20 25 30

His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His
35 40 45

Xaa Xaa Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro
50 55 60

Xaa Asp Leu Ala Xaa Glu Xaa Gly His Xaa Asp Xaa Xaa Xaa Tyr Leu
65 70 75 80

Arg Xaa Ala Xaa Gly Cys Ser Leu Cys Ser Ala Gly Trp Ser Leu Cys
85 90 95

Thr Ala Gly Asn Val Ala Gln Thr Asp Gly His Ser Phe Ser Ser Ser
100 105 110

Thr Pro Arg Ala Leu Glu Leu Arg Gly Gln Ser Gln Glu Gln Ser
115 120 125

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Val Ala Glu Ile Gly Xaa Gly Ala Tyr Gly Xaa Val Xaa Lys Ala Arg Asp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Val Xaa Lys Ala Arg Asp
1 5

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys Ala Arg Asp
1

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 960 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CGGAGAGGGA ATTCGGCACGA GGCAGCATG GAGCCTTCGG CTGACTGGCT GGCCACGGCC 60
GCGGCCCCGGG GTCGGGTAGA GGAGGTGCGG GCGCTGCTGG AGGCGGTGGC GCTGCCCCAA 120
CGCACCGAAT AGTTACGGTC GGAGGCCGAT CCAGGTCATG GATGATGGGC AGCGCCCCGA 180
GTGGCGGAGC TGCTGCTGCT CCACGGCGCG GAGCCCAACT GCGCCGACCC CGCCACTCTC 240

ACCCGACCCG TGCACCACGC TGCCCGGGAG GGCTTCTGGA CACGCTGGTG GTGCTGCACC 300
GGGCCGGGGC GCGGCTGGAC GTGCGCGATG CCTGGGGCCG TCTGCCCCGTG GACCTGGCTG 360
AGGAGCTGGG CCATCGCGAT GTCGCACGGT ACCTGCGCGC CCGTGCGGGG GGCACCAGAG 420
GCAGTAACCA TGCCCGCATA GATGCCGCGG AAGGTCCCTC AGACATCCCC GATTGAAAGA 480
ACCAGAGAGG CTCTGAGAAA CCTCGGGAAA CTTAGATCAT CAGTCACCGA AGGTCCTACA 540
GGGCCACAAC TGCCCCCGCC ACAACCCACC CCGCTTTCGT AGTTTTTCATT TAGAAAATAG 600
AGCTTTTAAA AATGTCCTGC CTTTTAACGT AGATATAAGC CTTCCCCCAC TACCGTAAAT 660
GTCCATTTAT ATCATTTTTT ATATATTCTT ATAAAAATGT AAAAAAGAA AAACACCGCT 720
TCTGCCTTTT CACTGTGTTG GAGTTTTCTG GAGTGAGCAC TCACGCCCTA AGCGCACATT 780
CATGTGGGCA TTTCTTGC GA CCTCGCAGC CTCCGGAAGC TGTCGACTTC ATGACAAGCA 840
TTTTGTGAAC TAGGGAAGCT CAGGGGGGTT ACTGGCTTCT CTTGAGTCAC ACTGCTAGCA 900
AATGGCAGAA CCAAAGCTCA AATAAAAATA AAATTATTTT CATTCAATTCA CTCAAAAAAA 960

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 334 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGNGGNAAGN TGTGGGGGAA AGTTTGGGGA TGGAANACCA ANCCCTCCTT TCNTTACCAA 60
ACNCTGGCTC TGNCGAGGCT NCNTCCGANT GGTNCCCCCG GGGGAGACCC AACCTGGGNC 120
GACTTCAGGG NTGCNACATT CATTCATAA GTGCTNGGAG NTAATANCAC CTCCTCCGAG 180
CANNGACAGG NTCGGAGGGG GCTCTTCCCC CANCACCGGA GGAAGAAAGA GGAGGGNCTN 240
CGGAGAGGGG GAGAACAGAC AACGGGCGGC GGGGAGCAGC ATGGATCCGG CGGCGGGGAG 300
CAGCATGGAN CCTTCGACTG ACTGACTGCC TCGC 334

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 368 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TCNCTTATTG NTAGGANATA ATAACACCTC CACCGATAAC TTCAC TTACA ACGTCCCNNT	60
TCCTGGAAAG ATACACAGCG TTCCCTCCAG AGGATTTGTG GGACAGGGTN GGAGNGGTCT	120
CTTCNCCAC CACCGGAGGA AGAAAGAGGA GGGGCTGNCT GTTCACCAGA GGGTGGGACG	180
GACCNCGTAC GCTCGNCGNC TNCGGAGAGG GGGAGAGCAT CANCGNCGN CGGGGAGCAA	240
CATGGAACCG NCGGCGGGGA GCAGCATGGA NCCTTCGGCT GACTGGCTGN CCACGNCCAC	300
GNCCCGGGGT CGGGTAGAGG AGGTGCGGNC GCTNCTGGAG GCGGGGNCTC TGNCCAACNC	360
GCTAAAN	368

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 404 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GACNNNTCC GGCCGGNGTC GGGTAGAGGA GGTGCGGGCG CTGCTGGAGG CGGGGGCGCT	60
GCCCAACGCA CCGAATAGTT ACGGTCGGAG GCCGATCCAG GTNNGGGTAG AGGGTCTGCA	120
GCGGGAGCAG GGGATGGCGG GCGACTCTGG AGGACGAAGT TTGCAGGGGA ATTGGAATCA	180
GGTAGCGCTT CGATTCTCCN GAAAAAGGGG AGGCTTCCTG GGGAGTTTTC AGAAGGGGTT	240
TGTAATCACA GACCTCTCC TGGCGACGTC CTGGGGGCTT GGGAAGCCAA GGAAGAGGAA	300
TNAGGAGCCA CGCGGTACG AGTCTCTCGA ATGCTGAGAA GATCTNAAGG GGGGAACATA	360
TTTGTATTAG CNTCCAAGTN TNCTCTNTAT CANATACAAA NTNC	404

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 401 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTCTNANCCC GGGTAGAGGG TCTGCAGCGG GAGCAGNNGA TGGCGGGCGA CTCTGGAGGA 60
CGAAGTTGGC AGGGGAATTG GAATCAGGTA GCGCTTCGAN TCTCCGAAA AAGGGGAGGC 120
TTCCTGGGGA GTTNNCAGAA GGGGTTTGTA ATCACAGNCC TCCNCCTGGC GACGCCCTGG 180
GGGGTTGGGA AGCCAAGGAA GAGGAATGAG GAGNCACGCG CNTACAGNTC TCTCGAATNC 240
TGANAAGATC TGAAGGGGGG AACATATTTG TATTAGNATN NAAGTATGCT CTTTATCAGA 300
TAGAAAATTC ACGAACGTGT GGNATAAAAA GGGAGTCTTA AAGAAATNTA AGATGTGCTG 360
GGACTACTTA GCCTCCAANA CACAGATNCC TGGATGGAGC T 401

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 459 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AAAANNAAAA AAAATCTCCC AGGCCTAACA TAATTNTCAG GAAAGAAATT TCAGTAGTTG 60
NATCTCAGGG GAAATACAGG AAGTTAGCCT GGAGTAAAG TCAGTGTGTC CCTGCCCCCTT 120
TGCTANATTG CCCGTGCCTC ACAGTGCTCT CTGCCTGTGA CGACAGCTCC NCAGAAGTTC 180
GGAGGATATA ATGGAATTCA TTGTGTACTG AAGAATGGAT AGAGAACTCA AGAAGGAAAT 240
TGGAAGCTGG AAGCAAATGT AGGGGTAATT AGACACCTGG GGCTTCTGTG GGGGTCTGCT 300
TGGCGGTGAG GGGGCTCTAC ACAAGCTTCC TTCCGTCAT GCCGNCCCCC ACCCTGGCTC 360
TGACCATTCT GTTCTCTCTG GCAGGTCATG ATGATGGGCA GCGCCCGAGG CGCGGAGCTG 420
CTGCTGCTCC ACGGCGCGGA GCCCACTGCT CCGACGCCG 459

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 390 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AANAAAAAAG AAATNGATAA NATAGAGGAA TGAACANATT AAAATCAAAA AACANAACAN 60
AGACATAATA AAAAACGAGA ATGTTCTAGA CNTAATCATA ATTATAAAGC TCAAGACTCA 120
TTGATATNAA GGADATTGAA GGGAAATCTT AACTAGCACA ANNGNATNAA AAAANAATTC 180
CCACGACACC GCCACTCTCA ACGCATCCGT GCTCGACACT GCCC GGGAGG TCNTCCTGGA 240
CACGCTGGTG GTNCTCCACC GGNCCGGGGC ACGTCTGGAC GTGCGCGATG CCTGGGNCCG 300
NCTACCCGTG GTACCTGACT GAGGACCTGG GCCATCCCGA TTTCGCNNGG TANCTCNNGN 360
GGCTGNNGGG GCCAANAGAG GNCANTACCC 390

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 214 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCTGCNACGA CCCCGCCACT CTCACCCGAC CCGTGCACGA CGCTGTCCGG GAGGGTTTCC 60
TGGACACGCT GGTGGTGCTG CACCGGGCCG GGGNGCGGTT GGACGTGCGC GATGCCTGGG 120
GCCGCCTNCC CGTGGNACCT GGTGAGGAG CTGGGNCATC GCGATGTCGC ACGGTACCTG 180
CGCGCGTTGC GGGGGGCACC AGAGGNNAGT NACC 214

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

NCTCTCACGG TGGGGAGGCC AACTGCGCCG AACCCGCCAC TCTACCCGA CCCGCGCACG 60
ACGGTGCCCG GGAGGGGTTT CTGGACACGC TGGTGGTGCT GCACCGGGCC GGGGCGCGGC 120
TGGACGTTTG NGATGCCTGG GGGNTCTNTC CGTNGNACCT GGCTGAAGAG CTGGNNCATC 180
GNGATGTCGC ACGGCCNCTG TGTGNGGNTG CGGGGGGCAC CATAGGTCAG TNTCC 235

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

NAAGTATGAG CGAAACNAAT TGTGGTTTGA GAANAGGNAA TCGTAGGGAA CTTCGGGATC 60
CCNCNGGGAN CNCCAGAACC TGAGNCGCCN ATTGGAAATN ACAAAC TGNC TGNATCACTC 120
CGNACCAGGT NCAAAAGATA CCTGGGGANG CGGGAAGGGA AAGACNACAT CNAGACCGCC 180
TTCGCNCCTN GGNATTGTGA GCAGCCTCTG AGACTCATTN ATATNACACT CTCGTNTTTC 240
TTCTTACAAC CCTGCGGNCC GCGCGGTCTG GCTTTCTCTG CCCTCCGCCG GGTGGACCTG 300
GAGCGCTTGA GCGGTCTGGC GCGCTGGAGC AGCCAGGCGG NCAGTGGACT AGCTGCTGGA 360
CCAGGGAGGT GTGGGAGAGC GGTGGCGGCG GGTACATGCA CGTGAAGCCA TTGCGAGAAC 420
TTTATCCATA AGTATTTCAA TACCGGTAGG GACGGCAAGA GAGGAGGGCG GGATGTGCCA 480
CACATCTTTG ACCTCAGGTT TCTAACGCCT GTTTTCTTTC TGCCCTCTGC AGACAACCCC 540
CGATTGAAAG AACCAGAGAG GCTCTGAGAA ACC 573

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 434 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CCCCATCGCG CTTGGGANT GTGAGCNACC ATTGAGACTC ATNAATATAG CACTCGTTTT 60
TCTTCTTGCA ACCCTGCCCN CCGCGCGGTC GCGCTNTCTC TGCCCTCCGC NGGGTGGACC 120
TGGAGCGAGC GCTTGAGCGG TCGGTCGGCG CNCCTGGANC AGCCAGGCGG GCAGTGGACT 180
ACCTNCTGGA CCAGGGACCT GTGGGAGAGC GTGNCGGCG GGTACATGCA CGTGAAGCCA 240
TTGCGAGAAC TTTATCCATA AGTATTTCAA TGCCGGTAGG GACGGCAAGA GAGGAGGGCG 300

GGATGTNCCA CACATCTTTG ACCTCAGGTT TCTAACGCCT GTTTTCTTTC TGCCCTCTGC 360
AGACATCCCC GATTGAAAGA ACCAGAGAGG CTCTGAGAAA CCTCCGAAA CTTAGNTCAT 420
CANTCGCCGN AAAA 434

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 502 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AGAAATTAGA TCATCAGTCA CCGATCCTCC TACAGGGNCA CAACTGNCCC CGCCACAACC 60
CACCCCGNTT TCGTAGTTTT CATTTAGAAA ATAGAGCTTT TAAAAATGTC CTGCCTTTTA 120
ACGTAGATAT ATGCCTTCCC CCACTACCGN AAATGTCCAT TTATATCATN TTTTATATAT 180
TCTTATAAAA ATGTAAAAAA GAAAAACACC GCTTCTGCCT TTCACTGTG TTGGAGTTTT 240
CTGGAGTGAG CACTCACGCC CTAAGCGCAC ATTCATGTGG GCATTTCTTG CGAGCCTCGC 300
AGNCTCCGGA AGCTGTGCGAC CTCGAGGGGG GGNCGGTAC CCAATTCGCC CTATAGTGAG 360
TCGTATTACA ATTCACTGGN CGNCGNTTTT ACAACGTCCG TGGACTGGGA AAACCCCGGN 420
GTTACCCAAC TTTAATCGNC TTGGAGGACA TCCCCCTTTT CGCCAGNTGG GGTTATAGNG 480
AAGAGGGCCN CACCNNTCGC CC 502

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 503 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CANCNATNTN CGGCATTTCT NGNGAGCCTC GTAGTCTCCG GATGNTGTG ACCTCGAGGG 60
GGGGNCCNGT ACCCAATTCG NCCTATNGTG AGTCGTNTTA CAATTCAC TG GCCCGCTTT 120
TNACAACGTC GNTGNACTGG GAAAACCCTG GTGTTACCCA ACTTNAATGT CCTTGNAGNA 180
CATCCCCCTT TNCGCCAGCT GGTGTAATAG CGANGAGGCC CGCACCGATC GCCCTTCCCA 240

ACAGTTGNGC AGCCTGAATG GCGAATGGAA ATTGTAAGCG TTAATATTTT GTTAAAATTC	300
GCGTTANATC NTCGGTTAAN TCAGCTCATN TTTTATCCAA TAGGCCGANA TCGGCANAAT	360
CCCCAATAAA TCAANAGAAT AGACCGAGAT AGGGTTGAGT GTCGTTCCAG TTNGGGAACA	420
NGAGTCCACT ATTAAAGANC GTAGNCTCNA ACGTCANAGG GCGAAAAACC NTNTTTCAGN	480
GGATTGGNCC ACTACGCNTA NCC	503

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 515 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CANCNATNTN CGGCATTTCT NGNGAGCCTC GTAGTCTCCG GATGNTGTCG ACCTCGAGGG	60
GGGGNCCNGT ACCCAATTCT NCCTATNGTG AGTCGTNTTA CAATTCACTG GCCGCCGTTT	120
TNACAACGTC GNTGNACTGG GAAAACCCTG GTGTTACCCA ACTTNAATCG CCTTGNAGNA	180
CATCCCCCTT TNCGCCAGCT GGTGTAATAG CGANGAGGCC CGCACCGATC GCCCTTCCCA	240
ACAGTTGNGC AGCCTGAATG GCGAATGGAA ATTGTAAGCG TTAATATTTT GTTAAAATTC	300
GCGTTANATC NTCGGTTAAN TCAGCTCATN TTTTATCCAA TAGGCCGANA TCGGCANAAT	360
CCCCAATAAA TCAANAGAAT AGACCGAGAT AGGGTTGAGT GTCGTTCCAG TTNGGGAACA	420
NGAGTCCACT ATTAAAGANC GTAGNCTCNA ACGTCANAGG GCGAAAAACC NTNTTTCAGN	480
GGATTGGNCC ACTACGCNTA NCCATCACCC TATTC	515

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 89 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu
 1 5 10 15
 His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val
 20 25 30
 His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg
 35 40 45 50
 Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp
 55 60 65
 Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg Tyr Leu Arg Ala Ala
 70 75 80 85
 Ala Gly Gly Thr

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 88 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu
 1 5 10 15
 His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val
 20 25 30
 His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg
 35 40 45 50
 Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp
 55 60 65
 Leu Ala Glu Glu Arg Gly His Arg Asp Val Ala Gly Tyr Leu Arg Thr Ala
 70 75 80 85
 Thr Gly Asp

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 85 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide